

AMENDMENTS TO THE CLAIMS

1. (Previously Presented) A method for rank ordering characteristic signatures of properties, said method comprising the steps of:

forming a plurality of characteristic signatures, each said characteristic signature being formed of values for a particular property having been measured from a plurality of samples taken from a heterogeneous tissue region, wherein the heterogeneous tissue region includes a first portion having at least first and second types of tissue, bordered by a second portion, said second portion considered to be devoid of the second type of tissue, wherein the plurality of samples have been taken from successive locations along a determined profile of locations through the heterogeneous tissue region, with at least one sample being taken from the second portion, and wherein each of said characteristic signatures are formed from different ones of said particular properties, respectively;

providing a trend profile of a second tissue measured property for the second type of tissue along the determined profile of locations through the heterogeneous tissue region;

performing statistical analysis on each of the plurality of characteristic signatures with regard to the provided trend profile; and

rank ordering the plurality of characteristic signatures based on proximity to the trend profile as determined by the statistical analysis.

2. (Previously Presented) The method of claim 1, further comprising the step of:
measuring the specific property for each of the plurality of samples for at least one of characteristic signatures.

3. (Original) The method of claim 1, further comprising the steps of:
providing the heterogeneous tissue region; and
taking the plurality of samples from the heterogeneous tissue region.

4. (Previously Presented) The method of claim 3, further comprising the step of:
measuring each specific property for each of the plurality of samples for each respective characteristic signature.

5. (Original) The method of claim 1, wherein the step of forming a plurality of characteristic signatures includes normalizing each of the plurality of characteristic signatures with respect to a baseline reference signature, said baseline reference signature corresponding to a measured property of a sample taken from the second portion.

6. (Original) The method of claim 1, wherein the step of performing statistical analysis includes:

comparing each of the plurality of characteristic signatures with the provided trend profile by curve-fitting to a statistical regression function, wherein said curve-fitting determines the degree of proximity of each of the plurality of characteristic signatures to the provided trend profile.

7. (Original) The method of claim 1, wherein the step of performing statistical analysis includes:

calculating a p-value with regard to each of the plurality of characteristic signatures, to test the null hypothesis between each of the plurality of characteristic signatures and the provided trend profile.

8. (Original) The method of claim 1, wherein the step of performing statistical analysis is done in one-, two- or three-dimensional space.

9. (Original) The method of claim 1, wherein the first type of tissue is healthy tissue.

10. (Original) The method of claim 1, wherein the second type of tissue is diseased tissue.

11. (Previously Presented) The method of claim 1, wherein one of the specific properties is an expression level of a gene.

12. (Previously Presented) The method of claim 2, wherein the step of measuring the specific property comprises measuring different specific properties across the samples to form a plurality of characteristic signatures by processing each of the plurality of samples using a microarray technique.

13. (Currently Amended) The method of claim ~~12~~ 13, wherein said processing comprises

processing each of the plurality of samples on a single two-color microarray, two single-color microarrays or both.

Claims 14 - 16. (Canceled)

17. (Currently Amended) A computer readable medium carrying one or more sequences of instructions for rank ordering characteristic signatures of properties measured from a plurality of samples taken from a heterogeneous region, wherein said computer readable medium is not a carrier wave or signal per se, wherein a first portion of the heterogeneous tissue region has at least first and second types of tissue and is bordered by a second portion of the heterogeneous tissue region, wherein the second portion is considered to be devoid of the second type of tissue, and wherein the plurality of samples have been taken from successive locations along a determined profile of locations through the heterogeneous tissue region, with at least one sample being taken from the second portion, wherein execution of one or more sequences of instructions by one or more processors causes the one or more processors to perform the steps of:

forming a plurality of characteristic signatures, each said characteristic signature being formed of values for a particular property having been measured from the plurality of samples;

providing a trend profile of a second tissue measured property of the second type of tissue along the determined profile of locations through the heterogeneous tissue region;

performing statistical analysis on each of the plurality of characteristic signatures with regard to the provided trend profile; and

rank ordering the plurality of characteristic signatures based on proximity to the trend profile as determined by the statistical analysis.

18. (Previously Presented) A system for rank ordering characteristic signatures of ~~cell~~ properties generated from tissue samples taken from a heterogeneous tissue region, wherein a first portion of the heterogeneous tissue region has at least first and second types of tissue and is bordered by a second portion of the heterogeneous tissue region, wherein the second portion is considered to be devoid of the second type of tissue, the system comprising:

means for providing a trend profile of a second tissue measured property of the second type of tissue along a determined profile of locations through the heterogeneous tissue region from which tissues samples are taken as the sources of the characteristic signatures;

means for performing statistical analysis on each of the plurality of characteristic signatures with regard to the provided trend profile; and

means for rank ordering the plurality of characteristic signatures based on proximity to the trend profile as determined by the statistical analysis.

19. (Previously Presented) The system of claim 18, further comprising means for forming the plurality of characteristic signatures based on measurements of values for a particular property measured from the plurality of samples, each of said characteristic signatures formed from values for a particular property different from the particular properties measured to form others of the characteristic signatures.

20. (Previously Presented) The system of claim 18, further comprising:
means for measuring at least one said specific property for each of the plurality of samples.

Claims 21-34. (Canceled)

35. (New) The method of claim 1, further comprising outputting a result of said method to at least one of a display or a user in a user readable format.

36. (New) The system of claim 18, further comprising means for outputting a result to at least one of a display or a user in a user readable format.

37. (New) The method of claim 1, wherein the second type of tissue comprises diseased tissue.

38. (New) The computer readable medium of claim 17, wherein the second type of tissue comprises diseased tissue.

39. (New) The system of claim 18, wherein the second type of tissue comprises diseased tissue.

40. (New) The method of claim 1, wherein a plurality of samples are taken from said first

portion.

41. (New) The computer readable medium method of claim 17, wherein a plurality of samples are taken from said first portion.

42. (New) The system of claim 18, wherein a plurality of samples are taken from said first portion.